

GG GCG CGA GCG CCT CAG CGC GGC CGC TCG CTC TCC CCC 38  
 Ala Arg Ala Pro Gln Arg Gly Arg Ser Leu Ser Pro  
 1 5 10  
 TCG AGG GAC AAA CTT TTC CCA AAC CCG ATC CGA GCC CTT 77  
 Ser Arg Asp Lys Leu Phe Pro Asn Pro Ile Arg Ala Leu  
 15 20 25  
 GGA CCA AAC TCG CCT GCG CCG AGA GCC GTC CGC GTA GAG 116  
 Gly Pro Asn Ser Pro Ala Pro Arg Ala Val Arg Val Glu  
 30 35  
 CGC TCC GTC TCC GGC GAG ATG TCC GAG CGC AAA GAA GGC 155  
 Arg Ser Val Ser Gly Glu Met Ser Glu Arg Lys Glu Gly  
 40 45 50  
 AGA GGC AAA GGG AAG GGC AAG AAG GAG CGA GCC TCC 194  
 Arg Gly Lys Gly Lys Gly Lys Lys Glu Arg Gly Ser  
 55 60  
 GGC AAG AAG CCG GAG TCC GCG GCG AGC CAG AGC CCA 233  
 Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser Pro  
 65 70 75  
 GCC TTG CCT CCC CGA TTG AAA GAG ATG AAA AGC CAG GAA 272  
 Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu  
 80 85 90  
 TCG GCT GCA GGT TCC AAA CTA GTC CTT CGG TGT GAA ACC 311  
 Ser Ala Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr  
 95 100  
 AGT TCT GAA TAC TCC TCT CTC AGA TTC AAG TGG TTC AAG 350  
 Ser Ser Glu Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys  
 105 110 115  
 AAT GGG AAT GAA TTG AAT CGA AAA AAC AAA CCA CAA AAT 389  
 Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn  
 120 125  
 ATC AAG ATA CAA AAA AAG CCA GGG AAG TCA GAA CTT CGC 428  
 Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg  
 130 135 140  
 ATT AAC AAA GCA TCA CTG GCT GAT TCT GGA GAG TAT ATG 467  
 Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met  
 145 150 155  
 TGC AAA GTG ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT 506  
 Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser  
 160 165

FIG. 1A

GCC AAT ATC ACC ATC GTG GAA TCA AAC GAG ATC ATC ACT 545  
 Ala Asn Ile Thr Ile Val Glu Ser Asn Glu Ile Ile Thr  
 170 175 180  
 GGT ATG CCA GCC TCA ACT GAA GGA GCA TAT GTG TCT TCA 584  
 Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr Val Ser Ser  
 185 190  
 GAG TCT CCC ATT AGA ATA TCA GTA TCC ACA GAA GGA GCA 623  
 Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala  
 195 200 205  
 AAT ACT TCT TCA TCT ACA TCT ACA TCC ACC ACT GGG ACA 662  
 Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Gly Thr  
 210 215 220  
 AGC CAT CTT GTA AAA TGT GCG GAG AAG GAG AAA ACT TTC 701  
 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe  
 225 230  
 TGT GTG AAT GGA GGG GAG TGC TTC ATG GTG AAA GAC CTT 740  
 Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu  
 235 240 245  
 TCA AAC CCC TCG AGA TAC TTG TGC AAG TGC CAA CCT GGA 779  
 Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Gln Pro Gly  
 250 255  
 TTC ACT GGA GCA AGA TGT ACT GAG AAT GTG CCC ATG AAA 818  
 Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro Met Lys  
 260 265 270  
 GTC CAA AAC CAA GAA AAG GCG GAG GAG CTG TAC CAG AAG 857  
 Val Gln Asn Gln Glu Lys Ala Glu Glu Leu Tyr Gln Lys  
 275 280 285  
 AGA GTG CTG ACC ATA ACC GGC ATC TGC ATC GCC CTC CTT 896  
 Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu  
 290 295  
 GTG GTC GGC ATC ATG TGT GTG GTG GCC TAC TGC AAA ACC 935  
 Val Val Gly Ile Met Cys Val Val Ala Tyr Cys Lys Thr  
 300 305 310  
 AAG AAA CAG CGG AAA AAG CTG CAT GAC CGT CTT CGG CAG 974  
 Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln  
 315 320  
 AGC CTT CGG TCT GAA CGA AAC AAT ATG ATG AAC ATT GCC 1013  
 Ser Leu Arg Ser Glu Arg Asn Asn Met Met Asn Ile Ala  
 325 330 335

AAT	GGG	CCT	CAC	CAT	CCT	AAC	CCA	CCC	CCC	GAG	AAT	GTC	1052
Asn	Gly	Pro	His	His	Pro	Asn	Pro	Pro	Pro	Glu	Asn	Val	
													350
													340
													345
CAG	CTG	GTG	AAT	CAA	TAC	GTA	TCT	AAA	AAC	GTC	ATC	TCC	1091
Gln	Leu	Val	Asn	Gln	Tyr	Val	Ser	Lys	Asn	Val	Ile	Ser	
													360
													355
AGT	GAG	CAT	ATT	GTT	GAG	AGA	GAA	GCA	GAG	ACA	TCC	TTT	1130
Ser	Glu	His	Ile	Val	Glu	Arg	Glu	Ala	Glu	Thr	Ser	Phe	
													375
													365
TCC	ACC	AGT	CAC	TAT	ACT	TCC	ACA	GCC	CAT	CAC	TCC	ACT	1169
Ser	Thr	Ser	His	Tyr	Thr	Ser	Thr	Ala	His	His	Ser	Thr	
													385
													380
ACT	GTC	ACC	CAG	ACT	CCT	AGC	CAC	AGC	TGG	AGC	AAC	GGA	1208
Thr	Val	Thr	Gln	Thr	Pro	Ser	His	Ser	Trp	Ser	Asn	Gly	
													400
													390
													395
CAC	ACT	GAA	AGC	ATC	CTT	TCC	GAA	AGC	CAC	TCT	GTA	ATC	1247
His	Thr	Glu	Ser	Ile	Leu	Ser	Glu	Ser	His	Ser	Val	Ile	
													415
													405
GTG	ATG	TCA	TCC	GTA	GAA	AAC	AGT	AGG	CAC	AGC	AGC	CCA	1286
Val	Met	Ser	Ser	Val	Glu	Asn	Ser	Arg	His	Ser	Ser	Pro	
													425
													420
ACT	GGG	GGC	CCA	AGA	GGA	CGT	CTT	AAT	GGC	ACA	GGA	GGC	1325
Thr	Gly	Gly	Pro	Arg	Gly	Arg	Leu	Asn	Gly	Thr	Gly	Gly	
													440
													430
CCT	CGT	GAA	TGT	AAC	AGC	TTC	CTC	AGG	CAT	GCC	AGA	GAA	1364
Pro	Arg	Glu	Cys	Asn	Ser	Phe	Leu	Arg	His	Ala	Arg	Glu	
													450
													445
ACC	CCT	GAT	TCC	TAC	CGA	GAC	TCT	CCT	CAT	AGT	GAA	AGG	1403
Thr	Pro	Asp	Ser	Tyr	Arg	Asp	Ser	Pro	His	Ser	Glu	Arg	
													465
													455
TAT	GTG	TCA	GCC	ATG	ACC	ACC	CCG	GCT	CGT	ATG	TCA	CCT	1442
Tyr	Val	Ser	Ala	Met	Thr	Thr	Pro	Ala	Arg	Met	Ser	Pro	
													480
													470
GTA	GAT	TTC	CAC	ACG	CCA	AGC	TCC	CCC	AAA	TCG	CCC	CCT	1481
Val	Asp	Phe	His	Thr	Pro	Ser	Ser	Pro	Lys	Ser	Pro	Pro	
													490
													485
TCG	GAA	ATG	TCT	CCA	CCC	GTG	TCC	AGC	ATG	ACG	GTG	TCC	1520
Ser	Glu	Met	Ser	Pro	Pro	Val	Ser	Ser	Met	Thr	Val	Ser	
													505
													500
													495

ATG CCT TCC ATG GCG GTC AGC CCC TTC ATG GAA GAA GAG 1559  
 Met Pro Ser Met Ala Val Ser Pro Phe Met Glu Glu Glu  
 510 515

AGA CCT CTA CTT CTC GTG ACA CCA CCA AGG CTG CGG GAG 1598  
 Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu Arg Glu  
 520 525 530

AAG AAG TTT GAC CAT CAC CCT CAG CAG TTC AGC TCC TTC 1637  
 Lys Lys Phe Asp His His Pro Gln Gln Phe Ser Ser Phe  
 535 540 545

CAC CAC AAC CCC GCG CAT GAC AGT AAC AGC CTC CCT GCT 1676  
 His His Asn Pro Ala His Asp Ser Asn Ser Leu Pro Ala  
 550 555

AGC CCC TTG AGG ATA GTG GAG GAT GAG GAG TAT GAA ACG 1715  
 Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr  
 560 565 570

ACC CAA GAG TAC GAG CCA GCC CAA GAG CCT GTT AAG AAA 1754  
 Thr Gln Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys  
 575 580

CTC GCC AAT AGC CGG CGG GCC AAA AGA ACC AAG CCC AAT 1793  
 Leu Ala Asn Ser Arg Arg Ala Lys Arg Thr Lys Pro Asn  
 585 590 595

GGC CAC ATT GCT AAC AGA TTG GAA GTG GAC AGC AAC ACA 1832  
 Gly His Ile Ala Asn Arg Leu Glu Val Asp Ser Asn Thr  
 600 605 610

AGC TCC CAG AGC AGT AAC TCA GAG AGT GAA ACA GAA GAT 1871  
 Ser Ser Gln Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp  
 615 620

GAA AGA GTA GGT GAA GAT ACG CCT TTC CTG GGC ATA CAG 1910  
 Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Gly Ile Gln  
 625 630 635

AAC CCC CTG GCA GCC AGT CTT GAG GCA ACA CCT GCC TTC 1949  
 Asn Pro Leu Ala Ala Ser Leu Glu Ala Thr Pro Ala Phe  
 640 645

CGC CTG GCT GAC AGC AGG ACT AAC CCA GCA GGC CGC TTC 1988  
 Arg Leu Ala Asp Ser Arg Thr Asn Pro Ala Gly Arg Phe  
 650 655 660

TCG ACA CAG GAA GAA ATC CAG G 2010  
 Ser Thr Gln Glu Glu Ile Gln  
 665 669

GG GAC AAA CTT TTC CCA AAC CCG ATC CGA GCC CTT GGA 38  
 Asp Lys Leu Phe Pro Asn Pro Ile Arg Ala Leu Gly  
 1 5 10

CCA AAC TCG CCT GCG CCG AGA GCC GTC CGC GTA GAG CGC 77  
 Pro Asn Ser Pro Ala Pro Arg Ala Val Arg Val Glu Arg  
 15 20 25

TCC GTC TCC GGC GAG ATG TCC GAG CGC AAA GAA GGC AGA 116  
 Ser Val Ser Gly Glu Met Ser Glu Arg Lys Glu Gly Arg  
 30 35

GGC AAA GGG AAG GGC AAG AAG AAG GAG CGA GGC TCC GGC 155  
 Gly Lys Gly Lys Gly Lys Lys Glu Arg Gly Ser Gly  
 40 45 50

AAG AAG CCG GAG TCC GCG GGC AGC CAG AGC CCA GCC 194  
 Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser Pro Ala  
 55 60

TTG CCT CCC CAA TTG AAA GAG ATG AAA AGC CAG GAA TCG 233  
 Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser  
 65 70 75

GCT GCA GGT TCC AAA CTA GTC CTT CGG TGT GAA ACC AGT 272  
 Ala Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser  
 80 85 90

TCT GAA TAC TCC TCT CTC AGA TTC AAG TGG TTC AAG AAT 311  
 Ser Glu Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys Asn  
 95 100

GGG AAT GAA TTG AAT CGA AAA AAC AAA CCA CAA AAT ATC 350  
 Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn Ile  
 105 110 115

AAG ATA CAA AAA AAG CCA GGG AAG TCA GAA CTT CGC ATT 389  
 Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile  
 120 125

AAC AAA GCA TCA CTG GCT GAT TCT GGA GAG TAT ATG TGC 428  
 Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys  
 130 135 140

AAA GTG ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT GCC 467  
 Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala  
 145 150 155

AAT ATC ACC ATC GTG GAA TCA AAC GAG ATC ATC ACT GGT 506  
 Asn Ile Thr Ile Val Glu Ser Asn Glu Ile Ile Thr Gly  
 160 165

FIG.2A

ATG CCA GCC TCA ACT GAA GGA GCA TAT GTG TCT TCA GAG 545  
 Met Pro Ala Ser Thr Glu Gly Ala Tyr Val Ser Ser Glu  
 170 175 180

TCT CCC ATT AGA ATA TCA GTA TCC ACA GAA GGA GCA AAT 584  
 Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala Asn  
 185 190

ACT TCT TCA TCT ACA TCT ACA TCC ACC ACT GGG ACA AGC 623  
 Thr Ser Ser Ser Thr Ser Thr Ser Thr Gly Thr Ser  
 195 200 205

CAT CTT GTA AAA TGT GCG GAG AAG GAG AAA ACT TTC TGT 662  
 His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys  
 210 215 220

GTG AAT GGA GGG GAG TGC TTC ATG GTG AAA GAC CTT TCA 701  
 Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser  
 225 230

AAC CCC TCG AGA TAC TTG TGC AAG TGC CCA AAT GAG TTT 740  
 Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe  
 235 240 245

ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC 779  
 Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe  
 250 255

TAC AAG CAT CTT GGG ATT GAA TTT ATG GAG GCG GAG GAG 818  
 Tyr Lys His Leu Gly Ile Glu Phe Met Glu Ala Glu Glu  
 260 265 270

CTG TAC CAG AAG AGA GTG CTG ACC ATA ACC GGC ATC TGC 857  
 Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys  
 275 280 285

ATC GCC CTC CTT GTG GTC GGC ATC ATG TGT GTG GTG GCC 896  
 Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val Ala  
 290 295

TAC TGC AAA ACC AAG AAA CAG CGG AAA AAG CTG CAT GAC 935  
 Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp  
 300 305 310

CGT CTT CGG CAG AGC CTT CGG TCT GAA CGA AAC AAT ATG 974  
 Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met  
 315 320

ATG AAC ATT GCC AAT GGG CCT CAC CAT CCT AAC CCA CCC 1013  
 Met Asn Ile Ala Asn Gly Pro His His Pro Asn Pro Pro  
 325 330 335

CCC GAG AAT GTC CAG CTG GTG AAT CAA TAC GTA TCT AAA 1052  
 Pro Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys  
 340 345 350

AAC GTC ATC TCC AGT GAG CAT ATT GTT GAG AGA GAA GCA 1091  
 Asn Val Ile Ser Ser Glu His Ile Val Glu Arg Glu Ala  
 355 360

GAG ACA TCC TTT TCC ACC AGT CAC TAT ACT TCC ACA GCC 1130  
 Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Ala  
 365 370 375

CAT CAC TCC ACT ACT GTC ACC CAG ACT CCT AGC CAC AGC 1169  
 His His Ser Thr Thr Val Thr Gln Thr Pro Ser His Ser  
 380 385

TGG AGC AAC GGA CAC ACT GAA AGC ATC CTT TCC GAA AGC 1208  
 Trp Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser  
 390 395 400

CAC TCT GTA ATC GTG ATG TCA TCC GTA GAA AAC AGT AGG 1247  
 His Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg  
 405 410 415

CAC AGC AGC CCA ACT GGG GGC CCA AGA GGA CGT CTT AAT 1286  
 His Ser Ser Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn  
 420 425

GGC ACA GGA GGC CCT CGT GAA TGT AAC AGC TTC CTC AGG 1325  
 Gly Thr Gly Gly Pro Arg Glu Cys Asn Ser Phe Leu Arg  
 430 435 440

CAT GCC AGA GAA ACC CCT GAT TCC TAC CGA GAC TCT CCT 1364  
 His Ala Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro  
 445 450

CAT AGT GAA AGG TAT GTG TCA GCC ATG ACC ACC CCG GCT 1403  
 His Ser Glu Arg Tyr Val Ser Ala Met Thr Thr Pro Ala  
 455 460 465

CGT ATG TCA CCT GTA GAT TTC CAC ACG CCA AGC TCC CCC 1442  
 Arg Met Ser Pro Val Asp Phe His Thr Pro Ser Ser Pro  
 470 475 480

AAA TCG CCC CCT TCG GAA ATG TCT CCA CCC GTG TCC AGC 1481  
 Lys Ser Pro Pro Ser Glu Met Ser Pro Pro Val Ser Ser  
 485 490

ATG ACG GTG TCC ATG CCT TCC ATG GCG GTC AGC CCC TTC 1520  
 Met Thr Val Ser Met Pro Ser Met Ala Val Ser Pro Phe  
 495 500 505

ATG	GAA	GAA	GAG	AGA	CCT	CTA	CTT	CTC	GTG	ACA	CCA	CCA	1559
Met	Glu	Glu	Glu	Arg	Pro	Leu	Leu	Leu	Val	Thr	Pro	Pro	
													515
AGG	CTG	CGG	GAG	AAG	TTT	GAC	CAT	CAC	CCT	CAG	CAG	1598	
Arg	Leu	Arg	Glu	Lys	Lys	Phe	Asp	His	His	Pro	Gln	Gln	
520													530
TTC	AGC	TCC	TTC	CAC	CAC	AAC	CCC	GCG	CAT	GAC	AGT	AAC	1637
Phe	Ser	Ser	Phe	His	His	Asn	Pro	Ala	His	Asp	Ser	Asn	
													545
AGC	CTC	CCT	GCT	AGC	CCC	TTG	AGG	ATA	GTG	GAG	GAT	GAG	1676
Ser	Leu	Pro	Ala	Ser	Pro	Leu	Arg	Ile	Val	Glu	Asp	Glu	
													555
GAG	TAT	GAA	ACG	ACC	CAA	GAG	TAC	GAG	CCA	GCC	CAA	GAG	1715
Glut	Tyr	Glu	Thr	Thr	Gln	Glu	Tyr	Glu	Pro	Ala	Gln	Glu	
													560
CCT	GTT	AAG	AAG	CTC	GCC	AAT	AGC	CGG	CGG	GCC	AAA	AGA	1754
Pro	Val	Lys	Lys	Leu	Ala	Asn	Ser	Arg	Arg	Arg	Ala	Lys	
													575
ACC	AAG	CCC	AAT	GGC	CAC	ATT	GCT	AAC	AGA	TTG	GAA	GTG	1793
Thr	Lys	Pro	Asn	Gly	His	Ile	Ala	Asn	Arg	Leu	Glu	Val	
													585
GAC	AGC	AAC	ACA	AGC	TCC	CAG	AGT	AAC	TCA	GAG	AGT	1832	
Asp	Ser	Asn	Thr	Ser	Ser	Gln	Ser	Ser	Asn	Ser	Glu	Ser	
													600
													605
													610

GAA	ACA	GAA	GAT	GAA	AGA	GTA	GGT	GAA	GAT	ACG	CCT	TTC	1871
Glu	Thr	Glu	Asp	Glu	Arg	Val	Gly	Glu	Asp	Thr	Pro	Phe	
													620
CTG	GGC	ATA	CAG	AAC	CCC	CTG	GCA	GCC	AGT	CTT	GAG	GCA	1910
Leu	Gly	Ile	Gln	Asn	Pro	Leu	Ala	Ala	Ser	Leu	Glu	Ala	
													635
ACA	CCT	GCC	TTC	CGC	CTG	GCT	GAC	AGC	AGG	ACT	AAC	CCA	1949
Thr	Pro	Ala	Phe	Arg	Leu	Ala	Asp	Ser	Arg	Thr	Asn	Pro	
													640
GCA	GGC	CGC	TTC	TCG	ACA	CAG	GAA	GAA	ATC	CAG	GCC	AGG	1988
Ala	Gly	Arg	Phe	Ser	Thr	Gln	Glu	Glu	Ile	Gln	Ala	Arg	
													655
CTG	TCT	ACT	GTA	ATT	GCT	AAC	CAA	GAC	CCT	ATT	GCT	GTA	2029
Leu	Ser	Ser	Val	Ile	Ala	Asn	Gln	Asp	Pro	Ile	Ala	Val	
													665
													670
													675
													2070
A AACCTAAATA AACACATAGA TTCACCTGTA AACTTTATT													
TTATATAATA AAGTATTCCA CCTTAAATTA AACATTATT TTTATTAG													2120
CACTCTGCA AATAGAAAAAC AGGAAAAAA CTTTATAAA TAAATATAT													2170
GTATGAAAAA ATGAAAAAA AAAA													2199

FIG. 2E

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GTGGCTGCGG GGCAATTGAA AAAGAGCCGG CGAGGAGTTC CCCGAAACTT 50  
GTTGGAACTC CGGGCTCGCG CGGAGGCCAG GAGCTGAGCG GCGGCGGCTG 100  
CCGGACGATG GGAGCGTGAG CAGGACGGTG ATAACCTCTC CCCGATCGGG 150  
TTGCGAGGGC GCCGGGCAGA GGCCAGGACG CGAGCCGCCA GCGGCGGGAC 200  
CCATCGACGA CTTCCCGGGG CGACAGGAGC AGCCCCGAGA GCCAGGGCGA 250  
GCGCCCGTTC CAGGTGGCCG GACCGCCCGC CGCGTCCGCG CCGCGCTCCC 300  
TGCAGGCAAC GGGAGACGCC CCCGCGCAGC GCGAGCGCCT CAGCGCGGCC 350  
GCTCGCTCTC CCCATCGAGG GACAAACTTT TCCCAAACCC GATCCGAGCC 400  
CTTGGACCAA ACTCGCCTGC GCCGAGAGCC GTCCGCGTAG AGCGCTCCGT 450  
CTCCGGCGAG ATG TCC GAG CGC AAA GAA GGC AGA GGC AAA 490  
Met Ser Glu Arg Lys Glu Gly Arg Gly Lys  
1 5 10  
GGG AAG GGC AAG AAG AAG GAG CGA GGC TCC GGC AAG AAG 529  
Gly Lys Gly Lys Lys Glu Arg Gly Ser Gly Lys Lys  
15 20  
CCG GAG TCC GCG GCG GGC AGC CAG AGC CCA GCC TTG CCT 568  
Pro Glu Ser Ala Ala Gly Ser Gln Ser Pro Ala Leu Pro  
25 30 35  
CCC CAA TTG AAA GAG ATG AAA AGC CAG GAA TCG GCT GCA 607  
Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala  
40 45  
GGT TCC AAA CTA GTC CTT CGG TGT GAA ACC AGT TCT GAA 646  
Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu  
50 55 60  
TAC TCC TCT CTC AGA TTC AAG TGG TTC AAG AAT GGG AAT 685  
Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn  
65 70 75  
GAA TTG AAT CGA AAA AAC AAA CCA CAA AAT ATC AAG ATA 724  
Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn Ile Lys Ile  
80 85

FIG. 3A

CAA AAA AAG CCA GGG AAG TCA GAA CTT CGC ATT AAC AAA 763  
 Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile Asn Lys  
 90 95 100

GCA TCA CTG GCT GAT TCT GGA GAG TAT ATG TGC AAA GTG 802  
 Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val  
 105 110

ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT GCC AAT ATC 841  
 Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile  
 115 120 125

ACC ATC GTG GAA TCA AAC GAG ATC ATC ACT GGT ATG CCA 880  
 Thr Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro  
 130 135 140

GCC TCA ACT GAA GGA GCA TAT GTG TCT TCA GAG TCT CCC 919  
 Ala Ser Thr Glu Gly Ala Tyr Val Ser Ser Glu Ser Pro  
 145 150

ATT AGA ATA TCA GTA TCC ACA GAA GGA GCA AAT ACT TCT 958  
 Ile Arg Ile Ser Val Ser Thr Glu Gly Ala Asn Thr Ser  
 155 160 165

TCA TCT ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT 997  
 Ser Ser Thr Ser Thr Ser Thr Gly Thr Ser His Leu  
 170 175

GTA AAA TGT GCG GAG AAG GAG AAA ACT TTC TGT GTG AAT 1036  
 Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
 180 185 190

GGA GGG GAG TGC TTC ATG GTG AAA GAC CTT TCA AAC CCC 1075  
 Gly Gly Cys Phe Met Val Lys Asp Leu Ser Asn Pro  
 195 200 205

TCG AGA TAC TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT 1114  
 Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly  
 210 215

GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AAG 1153  
 Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys  
 220 225 230

GCG GAG GAG CTG TAC CAG AAG AGA GTG CTG ACC ATA ACC 1192  
 Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr  
 235 240

GGC ATC TGC ATC GCC CTC CTT GTG GTC GGC ATC ATG TGT 1231  
 Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys  
 245 250 255

GTG GTG GCC TAC TGC AAA ACC AAG AAA CAG CGG AAA AAG 1270  
 Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys  
 260 265 270

FIG. 3B

CTG CAT GAC CGT CTT CGG CAG AGC CTT CGG TCT GAA CGA 1309  
 Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg  
 275 280

AAC AAT ATG ATG AAC ATT GCC AAT GGG CCT CAC CAT CCT 1348  
 Asn Asn Met Met Asn Ile Ala Asn Gly Pro His His Pro  
 285 290 295

AAC CCA CCC CCC GAG AAT GTC CAG CTG GTG AAT CAA TAC 1387  
 Asn Pro Pro Pro Glu Asn Val Gln Leu Val Asn Gln Tyr  
 300 305

GTA TCT AAA AAC GTC ATC TCC AGT GAG CAT ATT GTT GAG 1426  
 Val Ser Lys Asn Val Ile Ser Ser Glu His Ile Val Glu  
 310 315 320

AGA GAA GCA GAG ACA TCC TTT TCC ACC AGT CAC TAT ACT 1465  
 Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His Tyr Thr  
 325 330 335

TCC ACA GCC CAT CAC TCC ACT ACT GTC ACC CAG ACT CCT 1504  
 Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro  
 340 345

AGC CAC AGC TGG AGC AAC GGA CAC ACT GAA AGC ATC CTT 1543  
 Ser His Ser Trp Ser Asn Gly His Thr Glu Ser Ile Leu  
 350 355 360

TCC GAA AGC CAC TCT GTA ATC GTG ATG TCA TCC GTA GAA 1582  
 Ser Glu Ser His Ser Val Ile Val Met Ser Ser Val Glu  
 365 370

AAC AGT AGG CAC AGC AGC CCA ACT GGG GGC CCA AGA GGA 1621  
 Asn Ser Arg His Ser Ser Pro Thr Gly Gly Pro Arg Gly  
 375 380 385

CGT CTT AAT GGC ACA GGA GGC CCT CGT GAA TGT AAC AGC 1660  
 Arg Leu Asn Gly Thr Gly Pro Arg Glu Cys Asn Ser  
 390 395 400

TTC CTC AGG CAT GCC AGA GAA ACC CCT GAT TCC TAC CGA 1699  
 Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg  
 405 410

GAC TCT CCT CAT AGT GAA AGG TAT GTG TCA GCC ATG ACC 1738  
 Asp Ser Pro His Ser Glu Arg Tyr Val Ser Ala Met Thr  
 415 420 425

ACC CCG GCT CGT ATG TCA CCT GTA GAT TTC CAC ACG CCA 1777  
 Thr Pro Ala Arg Met Ser Pro Val Asp Phe His Thr Pro  
 430 435

AGC TCC CCC AAA TCG CCC CCT TCG GAA ATG TCT CCA CCC 1816  
 Ser Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro Pro  
 440 445 450

FIG. 3D

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ATT GCT GTA TAAAACCTA AATAAACACA TAGATTCAAC TGTAAAACCTT 2410  
Ile Ala Val  
635 637

TATTTTATAT AATAAAAGTAT TCCACCTTAA ATTAAACAAT TTATTTTATT 2460

TTAGCAGTTC TGCAAATAAA AAAAAAAA 2490

FIG. 3E

GCGCCTGCCT CCAACCTGCG GGCAGGGAGGT GGGTGGCTGC GGGGCAATTG 50  
 AAAAAGAGCC GGCAGGGAGT TCCCCGAAAC TTGTTGGAAC TCCGGGCTCG 100  
 CGCGGAGGCC AGGAGCTGAG CGCGGGCGGC TGCCGGACGA TGGGAGCGTG 150  
 AGCAGGACGG TGATAACCTC TCCCCGATCG GGTTGCGAGG GCGCCGGGCA 200  
 GAGGCCAGGA CGCGAGCCGC CAGCGGCGGG ACCCATCGAC GACTTCCCGG 250  
 GGCGACAGGA GCAGCCCCGA GAGCCAGGGC GAGCGCCCGT TCCAGGTGGC 300  
 CGGACCGCCC GCCGCGTCCG CGCCGCGCTC CCTGCAGGCA ACGGGAGACG 350  
 CCCCCGCGCA GCGCGAGCGC CTCAGCGCGG CCGCTCGCTC TCCCCATCGA 400  
 GGGACAAACT TTTCCAAAC CCGATCCGAG CCCTTGGACC AAACTCGCCT 450  
 GCGCCGAGAG CCGTCCGCGT AGAGCGCTCC GTCTCCGGCG AG ATG 495  
 Met 1  
 TCC GAG CGC AAA GAA GGC AGA GGC AAA GGG AAG GGC AAG 534  
 Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys  
 5 10  
 AAG AAG GAG CGA GGC TCC GGC AAG AAG CCG GAG TCC GCG 573  
 Lys Lys Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala  
 15 20 25  
 GCG GGC AGC CAG AGC CCA GCC TTG CCT CCC CAA TTG AAA 612  
 Ala Gly Ser Gln Ser Pro Ala Leu Pro Pro Gln Leu Lys  
 30 35 40  
 GAG ATG AAA AGC CAG GAA TCG GCT GCA GGT TCC AAA CTA 651  
 Glu Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu  
 45 50  
 GTC CTT CGG TGT GAA ACC AGT TCT GAA TAC TCC TCT CTC 690  
 Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu  
 55 60 65  
 AGA TTC AAG TGG TTC AAG AAT GGG AAT GAA TTG AAT CGA 729  
 Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg  
 70 75

FIG. 4A

AAA AAC AAA CCA CAA AAT ATC AAG ATA CAA AAA AAG CCA 768  
 Lys Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro  
 80 85 90

GGG AAG TCA GAA CTT CGC ATT AAC AAA GCA TCA CTG GCT 807  
 Gly Lys Ser Glu Leu Arg Ile Asn Lys Ala Ser Leu Ala  
 95 100 105

GAT TCT GGA GAG TAT ATG TGC AAA GTG ATC AGC AAA TTA 846  
 Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu  
 110 115

GGA AAT GAC AGT GCC TCT GCC AAT ATC ACC ATC GTG GAA 885  
 Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu  
 120 125 130

TCA AAC GAG ATC ATC ACT GGT ATG CCA GCC TCA ACT GAA 924  
 Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu  
 135 140

GGA GCA TAT GTG TCT TCA GAG TCT CCC ATT AGA ATA TCA 963  
 Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser  
 145 150 155

GTA TCC ACA GAA GGA GCA AAT ACT TCT TCA TCT ACA TCT 1002  
 Val Ser Thr Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser  
 160 165 170

ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA AAA TGT GCG 1041  
 Thr Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala  
 175 180

GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC 1080  
 Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys  
 185 190 195

TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG 1119  
 Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu  
 200 205

TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA 1158  
 Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln  
 210 215 220

AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC 1197  
 Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro  
 225 230 235

TTT CTG TCT CTG CCT GAA TAGGA GCATGCTCAG TTGGTGCTGC 1240  
 Phe Leu Ser Leu Pro Glu  
 240 241

TTTCTTGTG CTGCATCTCC CCTCAGATTG CACCTAGAGC TAGATGTGTC 1290

TTACCCAGATC TAATATTGAC TGCCTCTGCC TGTGCGATGA GAACATTAAC 1340  
AAAAGCAATT GTATTACTTC CTCTGTTCGC GACTAGTTGG CTCTGAGATA 1390  
CTAATAGGTG TGTGAGGGCTC CGGATGTTTC TGGAATTGAT ATTGAATGAT 1440  
GTGATACAAA TTGATAGTCA ATATCAAGCA GTGAAATATG ATAATAAAGG 1490  
CATTTCAAAG TCTCACTTTT ATTGATAAAA TAAAAATCAT TCTACTGAAC 1540  
AGTCCATCTT CTTTATACAA TGACCACATC CTGAAAAGGG TGTTGCTAAG 1590  
CTGTAACCGA TATGCACTTG AAATGATGGT AAGTTAATT TGATTCAGAA 1640  
TGTGTTATTT GTCACAAATA AACATAATAA AAGGAGTTCA GATGTTTTC 1690  
TTCATTAACC AAAAAAAAAA AAAAAA 1715

FIG. 4C

GAGGCGCCTG CCTCCAACCT GCAGGGCGGGGA GGTGGGTGGC TGCAGGGCAA 50  
 TTGAAAAAGA GCCGGCGAGG AGTTCCCCGA AACTTGTGTTGG AACTCCGGGC 100  
 TCGCGCGGGAG GCCAGGAGCT GAGCGGGCGGC GGCTGCCGGA CGATGGGAGC 150  
 GTGAGCAGGA CGGTGATAAC CTCTCCCCGA TCAGGGTTGCG AGGGCGCCGG 200  
 GCAGAGGCCA GGACGCGAGC CGCCAGCGGC GGGACCCATC GACGACTTCC 250  
 CGGGGCGACA GGAGCAGCCC CGAGAGCCAG GGCGAGCGCC CGTTCCAGGT 300  
 GCCCGGACCG CCCGCCGCGT CCGCGCCGCG CTCCCTGCAG GCAACGGGAG 350  
 ACGCCCCCGC GCAGCGCGAG CGCCTCAGCG CGGCCGCTCG CTCTCCCCAT 400  
 CGAGGGACAA ACTTTCCCA AACCCGATCC GAGCCCTTGG ACCAAACTCG 450  
 CCTGCGCCGA GAGCCGTCCG CGTAGAGCGC TCCGTCTCCG GCGAG AT 497  
 Met  
 1  
 G TCC GAG CGC AAA GAA GGC AGA GGC AAA GGG AAG GGC AAG 537  
 Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys  
 5 10  
 AAG AAG GAG CGA GGC TCC GGC AAG AAG CCG GAG TCC GCG 576  
 Lys Lys Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala  
 15 20 25  
 GCG GGC AGC CAG AGC CCA GCC TTG CCT CCC CAA TTG AAA 615  
 Ala Gly Ser Gln Ser Pro Ala Leu Pro Pro Gln Leu Lys  
 30 35 40  
 GAG ATG AAA AGC CAG GAA TCG GCT GCA GGT TCC AAA CTA 654  
 Glu Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu  
 45 50  
 GTC CTT CGG TGT GAA ACC AGT TCT GAA TAC TCC TCT CTC 693  
 Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu  
 55 60 65  
 AGA TTC AAG TGG TTC AAG AAT GGG AAT GAA TTG AAT CGA 732  
 Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg  
 70 75

*FIG. 5A*

AAA AAC AAA CCA CAA AAT ATC AAG ATA CAA AAA AAG CCA 771  
 Lys Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro  
 80 85 90

GGG AAG TCA GAA CTT CGC ATT AAC AAA GCA TCA CTG GCT 810  
 Gly Lys Ser Glu Leu Arg Ile Asn Lys Ala Ser Leu Ala  
 95 100 105

GAT TCT GGA GAG TAT ATG TGC AAA GTG ATC AGC AAA TTA 849  
 Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu  
 110 115

GGA AAT GAC AGT GCC TCT GCC AAT ATC ACC ATC GTG GAA 888  
 Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu  
 120 125 130

TCA AAC GAG ATC ATC ACT GGT ATG CCA GCC TCA ACT GAA 927  
 Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu  
 135 140

GGA GCA TAT GTG TCT TCA GAG TCT CCC ATT AGA ATA TCA 966  
 Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser  
 145 150 155

GTA TCC ACA GAA GGA GCA AAT ACT TCT TCA TCT ACA TCT 1005  
 Val Ser Thr Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser  
 160 165 170

ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA AAA TGT GCG 1044  
 Thr Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala  
 175 180

GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC 1083  
 Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys  
 185 190 195

TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG 1122  
 Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu  
 200 205

TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA 1161  
 Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln  
 210 215 220

AAC TAC GTA ATG GCC AGC TTC TAC AAG GCG GAG GAG CTG 1200  
 Asn Tyr Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu  
 225 230 235

TAC CAG AAG AGA GTG CTG ACC ATA ACC GGC ATC TGC ATC 1239  
 Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile  
 240 245

GCC CTC CTT GTG GTC GGC ATC ATG TGT GTG GTG GCC TAC 1278  
 Ala Leu Leu Val Val Gly Ile Met Cys Val Val Ala Tyr  
 250 255 260

TGC AAA ACC AAG AAA CAG CGG AAA AAG CTG CAT GAC CGT 1317  
 Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg  
 265 270

CTT CGG CAG AGC CTT CGG TCT GAA CGA AAC AAT ATG ATG 1356  
 Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met Met  
 275 280 285

AAC ATT GCC AAT GGG CCT CAC CAT CCT AAC CCA CCC CCC 1395  
 Asn Ile Ala Asn Gly Pro His His Pro Asn Pro Pro Pro  
 290 295 300

GAG AAT GTC CAG CTG GTG AAT CAA TAC GTA TCT AAA AAC 1434  
 Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn  
 305 310

GTC ATC TCC AGT GAG CAT ATT GTT GAG AGA GAA GCA GAG 1473  
 Val Ile Ser Ser Glu His Ile Val Glu Arg Glu Ala Glu  
 315 320 325

ACA TCC TTT TCC ACC AGT CAC TAT ACT TCC ACA GCC CAT 1512  
 Thr Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Ala His  
 330 335

CAC TCC ACT ACT GTC ACC CAG ACT CCT AGC CAC AGC TGG 1551  
 His Ser Thr Thr Val Thr Gln Thr Pro Ser His Ser Trp  
 340 345 350

AGC AAC GGA CAC ACT GAA AGC ATC CTT TCC GAA AGC CAC 1590  
 Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His  
 355 360 365

TCT GTA ATC GTG ATG TCA TCC GTA GAA AAC AGT AGG CAC 1629  
 Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His  
 370 375

AGC AGC CCA ACT GGG GGC CCA AGA GGA CGT CTT AAT GGC 1668  
 Ser Ser Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly  
 380 385 390

ACA GGA GGC CCT CGT GAA TGT AAC AGC TTC CTC AGG CAT 1707  
 Thr Gly Gly Pro Arg Glu Cys Asn Ser Phe Leu Arg His  
 395 400

GCC AGA GAA ACC CCT GAT TCC TAC CGA GAC TCT CCT CAT 1746  
 Ala Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His  
 405 410 415

AGT GAA AGG TAAAAA CCGAAGGCAA AGCTACTGCA GAGGAGAAC 1790  
 Ser Glu Arg  
 420

*FIG. 5C*

TCAGTCAGAG AATCCCTGTG AGCACCTGCG GTCTCACCTC AGGAAATCTA 1840  
CTCTAACAG AATAAGGGGC GGCAGTTACC TGTTCTAGGA GTGCTCCTAG 1890  
TTGATGAAGT CATCTCTTG TTTGACGGAA CTTATTTCTT CTGAGCTTCT 1940  
CTCGTCGTCC CAGTGACTGA CAGGCAACAG ACTCTTAAAG AGCTGGGATG 1990  
CTTGATGCG GAAGGTGCAG CACATGGAGT TTCCAGCTCT GGCCATGGGC 2040  
TCAGACCCAC TCGGGGTCTC AGTGTCTCA GTTGTAACAT TAGAGAGATG 2090  
GCATCAATGC TTGATAAGGA CCCTTCTATA ATTCCAATTG CCAGTTATCC 2140  
AAACTCTGAT TCGGTGGTCG AGCTGGCCTC GTGTTCTTAT CTGCTAACCC 2190  
TGTCTTACCT TCCAGCCTCA GTTAAGTCAA ATCAAGGGCT ATGTCATTGC 2240  
TGAATGTCAT GGGGGCAAC TGCTTGCCCT CCACCTATA GTATCTATTT 2290  
TATGAAATTCAAGAAGGGATGAATAAAATA AATCTCTTGG ATGCTGCGTC 2340  
TGGCAGTCTT CACGGGTGGT TTTCAAAGCA GAAAAAAA AAAAAAAA 2390  
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A 2431

FIG. 5D

16	1	MSE	ERKE	GRG	KGK	KKER	GSG	KP	ES	AAG	SQ	SPAL	PP	PR	L	KEM	K	SQ	ES	AAG
11	1	MSE	ERKE	GRG	KGK	KKER	GSG	KP	ES	AAG	SQ	SPAL	PP	QL	KEM	K	SQ	ES	AAG	
76	1	MSE	ERKE	GRG	KGK	KKER	GSG	KP	ES	AAG	SQ	SPAL	PP	QL	KEM	K	SQ	ES	AAG	
84	1	MSE	ERKE	GRG	KGK	KKER	GSG	KP	ES	AAG	SQ	SPAL	PP	QL	KEM	K	SQ	ES	AAG	
78	1	MSE	ERKE	GRG	KGK	KKER	GSG	KP	ES	AAG	SQ	SPAL	PP	QL	KEM	K	SQ	ES	AAG	

16	51	SKLVLRCETSSLEYSSSLR	WFKNGNELNRK	NKPQNIKIQKKPGKSEL	SEL	RIN
11	51	SKLVLRCETSSLEYSSSLR	WFKNGNELNRK	NKPQNIKIQKKPGKSEL	SEL	RIN
76	51	SKLVLRCETSSLEYSSSLR	WFKNGNELNRK	NKPQNIKIQKKPGKSEL	SEL	RIN
84	51	SKLVLRCETSSLEYSSSLR	WFKNGNELNRK	NKPQNIKIQKKPGKSEL	SEL	RIN
78	51	SKLVLRCETSSLEYSSSLR	WFKNGNELNRK	NKPQNIKIQKKPGKSEL	SEL	RIN

16	101	KASLADSGEY	MCKV	ISKL	GND	SAS	AN	IT	IVES	NE	!	IT	GMP	AST	E	GAY	VSS
11	101	KASLADSGEY	MCKV	ISKL	GND	SAS	AN	IT	IVES	NE	!	IT	GMP	AST	E	GAY	VSS
76	101	KASLADSGEY	MCKV	ISKL	GND	SAS	AN	IT	IVES	NE	!	IT	GMP	AST	E	GAY	VSS
84	101	KASLADSGEY	MCKV	ISKL	GND	SAS	AN	IT	IVES	NE	!	IT	GMP	AST	E	GAY	VSS
78	101	KASLADSGEY	MCKV	ISKL	GND	SAS	AN	IT	IVES	NE	!	IT	GMP	AST	E	GAY	VSS

16	151	E	SPIRISVSTEGANTSSSTS	TTGTSHLVKCAEKEKTFCVNGGECFMVK
11	151	E	SPIRISVSTEGANTSSSTS	TTGTSHLVKCAEKEKTFCVNGGECFMVK
76	151	E	SPIRISVSTEGANTSSSTS	TTGTSHLVKCAEKEKTFCVNGGECFMVK
84	151	E	SPIRISVSTEGANTSSSTS	TTGTSHLVKCAEKEKTFCVNGGECFMVK
78	151	E	SPIRISVSTEGANTSSSTS	TTGTSHLVKCAEKEKTFCVNGGECFMVK

FIG. 6A

16	201	DLSNPSRYLCKCQPGFTGARCTEN	VPMKVQNQ	- - -	EKAEEELYQKRVLT
11	201	DLSNPSRYLCKCQPNNEFTGDR	CQNYVMASFYK	HLGIEFME	AEEELYQKRVLT
76	201	DLSNPSRYLCKCPNEFTGDR	CQNYVMASFYK	- - -	AEELYQKRVLT
84	201	DLSNPSRYLCKCPNEFTGDR	CQNYVMASFYK	- - -	AEELYQKRVLT
78	201	DLSNPSRYLCKCPNEFTGDR	CQNYVMASFY	STSTPFLSLPE	
16	246	ITGICICIAALLVVGIMCVVAYC	KTKKQRK	KLHDRLRQSLRSE	ERNNMNMNIA
11	251	ITGICICIAALLVVGIMCVVAYC	KTKKQRK	KLHDRLRQSLRSE	ERNNMNMNIA
76	243	ITGICICIAALLVVGIMCVVAYC	KTKKQRK	KLHDRLRQSLRSE	ERNNMNMNIA
84	243	ITGICICIAALLVVGIMCVVAYC	KTKKQRK	KLHDRLRQSLRSE	ERNNMNMNIA
16	296	PHHPNPPENVQLVNQYVSKNV	ISSEHIV	IREAETSF	STSHYTS
11	301	PHHPNPPENVQLVNQYVSKNV	ISSEHIV	IREAETSF	STSHYTS
76	293	PHHPNPPENVQLVNQYVSKNV	ISSEHIV	IREAETSF	STSHYTS
84	293	PHHPNPPENVQLVNQYVSKNV	ISSEHIV	IREAETSF	STSHYTS
16	346	TVTQTPSHSWNGHTE	SILSESHSVIVM	SSPTGGP	RGRNLNGT
11	351	TVTQTPSHSWNGHTE	SILSESHSVIVM	SSPTGGP	RGRNLNGT
76	343	TVTQTPSHSWNGHTE	SILSESHSVIVM	SSPTGGP	RGRNLNGT
84	343	TVTQTPSHSWNGHTE	SILSESHSVIVM	SSPTGGP	RGRNLNGT

FIG. 6B

16	396	GGPRECONSFLRHARET PDSYR DSPH SERYV S AMTT PARMSPVDFHTPSSP
11	401	GGPRECONSFLRHARET PDSYR DSPH SERYV S AMTT PARMSPVDFHTPSSP
76	393	GGPRECONSFLRHARET PDSYR DSPH SERYV S AMTT PARMSPVDFHTPSSP
84	393	GGPRECONSFLRHARET PDSYR DSPH SERYV S AMTT PARMSPVDFHTPSSP
16	446	KSPPSEMSPPPVSSMTVSMPSMAVSPFMEEEERPLLLVTPPRLREKKFDHHHP
11	451	KSPPSEMSPPPVSSMTVSMPSMAVSPFMEEEERPLLLVTPPRLREKKFDHHHP
76	443	KSPPSEMSPPPVSSMTVSKPSPMAVSPFMEEEERPLLLVTPPRLREKKFDHHHP
16	496	QQFSSFFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPQAQEPVKKLANSR
11	501	QQFSSFFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPQAQEPVKKLANSR
76	493	QQFSSFFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPQAQEPVKKLANSR
16	546	RAKRTKPNNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNPL
11	551	RAKRTKPNNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNPL
76	543	RAKRTKPNNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNPL
16	596	AASLEATPAFRLADSRTNPAGRFS TQEEIQ-----
11	601	AASLEATPAFRLADSRTNPAGRFS TQEEIQARLSSVIANQDPIAV
76	593	AASLEATPAFRLADSRTNPAGRFS TQEEIQARLSSVIANQDPIAV

FIG. 6C

1 GGGTACCATGGGTGGTGGCGCGTTCCCGCCTGAGCGCAACTAGCGGC  
 51 GGGTCGTGGGCACCTCCAGAAAAGATCCCGCACCATCCTCCAGGATCCAA  
 101 TGGCCTTGGAGAGAGGGCTGCAGGGCCACGGACATTGCTGACTCTCAG  
 151 AACGTGCTGACATGGAGCCAGGTAGACTGAAATTATCATGTGTCCAAATT  
 201 AAAATTGCATACTTCAAGGATTATTGAAGGACTATTCTTAGACCCCTTT  
 251 AAGAAGATTAAAGAAAAACACTCGGCCCTGAGTGCAGGAGGACCCCTG  
 301 TTTGTGGATGTGGAGGGAGCGCGGGCCGGAGGCCATGGACGTGAAGGAGAG  
 1 M D V K E R  
 351 GAAGCCTTACCGCTCGCTGACCCGGCGCCGACGCCGAGCGCCGCTACA  
 7 K P Y R S L T R R R D A E R R Y T  
 401 CCAGCTCGTCCGGACAGCGAGGGAGGGCAAAGCCCCGAGAAATCGTAC  
 24 S S S A D S E E G K A P Q K S Y  
 451 AGCTCCAGCGAGACCCCTGAAGGCCTACGACCAGGACGCCGCTAGCCTA  
 40 S S S E T L K A Y D Q D A R L A Y  
 501 TGGCAGCCCGTCAAGGACATTGTGCCGCAGGAGGCCAGGAATTCTGCC  
 57 G S R V K D I V P Q E A E E F C R  
 551 GCACAGGTGCCAACTTCACCCCTGCCGGAGCTGGGCTGGAAGAAGTAACG  
 74 T G A N F T L R E L G L E E V T  
 601 CCCCTCACGGGACCCCTGTACCGGACAGACATTGGCCTCCCCACTGCC  
 90 P P H G T L Y R T D I G L P H C G  
 651 CTACTCCATGGGGCTGGCTCTGATGCCGACATGGAGGCTGACACGGTGC  
 107 Y S M G A G S D A D M E A D T V L  
 701 TGTCCTGAGCACCCCGTGCCTGTGGGCCGGAGCACACGGTCAGGG  
 124 S P E H P V R L W G R S T R S G  
 751 CGCAGCTCCTGCCTGTCCAGCCGGCAATTCCAATCTCACACTCACCGA  
 140 R S S C L S S R A N S N L T L T D  
 801 CACCGAGCATGAAAACACTGAGACTGATCATCCGGCGGCCTGCAGAAC  
 157 T E H E N T E T D H P G G L Q N H  
 851 ACGCGCGGCTCCGGACGCCGCCGCCGCTCTGCACGCCACACCCCC  
 174 A R L R T P P P L S H A H T P  
 901 AACCCAGCACCGCGGCCTCCATTAACTCCCTGAACCGGGCAACTTCAC  
 190 N Q H H A A S I N S L N R G N F T  
 951 GCCGAGGAGCAACCCAGCCGGCCCCACGGACCACTCGCTCTCCGGAG  
 207 P R S N P S P A P T D H S L S G E  
 1001 AGCCCCCTGCCGGCGCCAGGAGCCTGCCACGCCAGGAGAACTGG  
 224 P P A G G A Q E P A H A Q E N W  
 1051 CTGCTAACAGCAACATCCCCCTGGAGACCAAGAAACCTAGGCAAGCAGCC  
 240 L L N S N I P L E T R N L G K Q P

FIG. 7A

2001 CACCACTGCCATTGCCTGCCTCCCCGATTGAAAGAGATGAAAAGCCAGG  
 557 T T A I A L P P R L K E M K S Q E  
  
 2051 AATCGGCTGCAGGTTCCAAACTAGTCCTCGGTGTGAAACCCAGTCTGAA  
 574 S A A G S K L V L R C E T S S E  
  
 2101 TACTCCTCTCTCAGATTCAAGTGGTTCAAGAATGGGAATGAATTGAATCG  
 590 Y S S L R F K W F K N G N E L N R  
  
 2151 AAAAAACAAACACACAAATATCAAGATACAAAAAAAGCCAGGGAAGTCAG  
 607 K N K P Q N I K I Q K K P G K S E  
  
 2201 AACTTCGCATTAACAAAGCATCACTGGCTGATTCTGGAGAGTATATGTGC  
 624 L R I N K A S L A D S G E Y M C  
 • •  
 2251 AAAGTGATCAGCAAATTAGGAAATGACAGTCGCTCTGCCAATATCACCAT  
 640 K V I S K L G N D S A S A N I T I  
  
 2301 CGTGAATCAAACGAGATCATCACTGGTATGCCAGCCTCAACTGAAGGAG  
 657 V E S N E I I T G M P A S T E G A  
  
 2351 CATATGTGTCTTCAGAGTCTCCATTAGAATATCAGTATCCACAGAAGGA  
 674 Y V S S E S P I R I S V S T E G  
 •  
 2401 GCAAATACTTCTTCATCTACATCTACATCCACCACTGGGACAAGCCATCT  
 690 A N T S S S T S T S T T G T S H L  
  
 2451 TGTAATGTGCGGAGAAGGGAGAAACTTTCTGTGTGAATGGACGGGAGT  
 707 V K (C) A E K E K T F (C) V N G G E (C)  
  
 2501 GCTTCATGGTGAAGACCTTCAAAACCCCTCGAGATACTTGTGCAAGTGC  
 724 F M V K D L S N P S R Y L (C) K (C)  
  
 2551 CCAAATGAGTTTACTGGTGTGCCTGCCTGGCAAGCT  
 740 P N E F T G D R (C) Q N Y V M A S F  
  
 2601 CTACAGTACGTCCACTCCCTTCTGTCTGCCTGAATAGGAGCATGCTC  
 757 Y S T S T P F L S L P E  
  
 2651 AGTTGGTGCTGCTTCTTGTGCTGCATCTCCCTCAGATTCCACCTAGA  
  
 2701 GCTAGATGTGTCTTACCAAGATCTAATATTGACTGCCCTGCGCAT  
 2751 GAGAACATTAACAAAGCAATTGTATTACTTCCTCTGTTGCGACTAGTT  
 2801 GGCTCTGAGATACTAATAGGTGTGAGGCTCCGGATGTTCTGGAATTG  
 2851 ATATTGAATGATGTGATACAAATTGATAGTCAATATCAAGCAGTGAATA  
 2901 TGATAATAAAAGGCATTCAAAGTCTCACTTTATGATAAAATAAAATC  
 2951 ATTCTACTGAACAGTCCATCTCTTATACAATGACCACATCCTGAAAAG  
 3001 GGTGTTGCTAAGCTGAACCGATATGCACCTGAAATGATGGTAAGTTAAT  
 3051 TTTGATTCAAGAATGTGTTATGTCACAAATAACATAATAAAAGGAAAA  
 3101 AAAAAAA

FIG. 7B

1101 ATTCCCTAGGGACATTGCAGGACAAACCTCATTGAGATGGACATTCTCGGCG  
 257 F L G T L Q D N L I E M D I L G A  
  
 1151 CCTCCCGCCATGATGGGGCTTACAGTGACGGGCACTTCCTCTTCAAGCCT  
 274 S R H D G A Y S D G H F L F K P  
  
 1201 GGAGGCACCTCCCCGCTCTCTGCACCACATCACCAAGGGTACCCACTGAC  
 290 G G T S P L F C T T S P G Y P L T  
  
 1251 GTCCAGCACAGTGTACTCTCCTCCGCCCCGACCCCTGCCCGCAGCACCT  
 307 S S T V Y S P P P R P L P R S T F  
  
 1301 TCGCCCGGCCGGCCTTAACCTCAAGAAGCCCTCCAAGTACTGTAAGTGG  
 324 A R P A F N L K K P S K Y C N W  
  
 1351 AAGTGCAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGGTCATCCT  
 340 K C A A L S A I V I S A T L V I L  
  
 1401 GCTGGCATACTTGTGGCCATGCACCTGTTGGCTAAACTGGCACCTGC  
 357 L A Y F V A M H L F G L N W H L Q  
  
 1451 AGCCGATGGAGGGCAGATGTATGAGATCACGGAGGACACAGCCAGCAGT  
 374 P M E G Q M Y E I T E D T A S S  
  
 1501 TGGCCTGTGCCAACCGACGTCTCCCTATACCCCTCAGGGGGCACTGGCTT  
 390 W P V P T D V S L Y P S G G T G L  
  
 1551 AGAGACCCCTGACAGGAAAGGCAAAGGAACCACAGAAGGAAAGCCCAGTA  
 407 E T P D R K G K G T T E G K P S S  
  
 1601 GTTCTTCCAGAGGACAGTTCATAGATTCTGGAGAAATTGATGTGGGA  
 424 F F P E D S F I D S G E I D V G  
  
 1651 AGGCAGCTCCCAGAAGATTCCCTGGCACTTCTGGAGATCTCAAGT  
 440 R R A S Q K I P P G T F W R S Q V  
  
 1701 GTTCATAGACCATCCTGTGCATCTGAAATTCAATGTGTCTCTGGAAAGG  
 457 F I D H P V H L K F N V S L G K A  
  
 1751 CAGCCCTGGTTGGCATTATGGCAGAAAAGGCCTCCCTCCTCACATACA  
 474 A L V G I Y G R K G L P P S H T  
  
 1801 CAGTTGACTTGTGGAGCTGCTGGATGGCAGGGCTCCAAACCCAGGA  
 490 Q F D F V E L L D G R R L L T Q E  
  
 1851 GGCGCGGAGCCTAGAGGGACCCCGGCCAGTCTGGGGAACTGTGCC  
 507 A R S L E G T P R Q S R G T V P P  
  
 1901 CCTCCAGCCATGAGACAGGGCTCATCCAGTATTGGATTCAAGGAATCTGG  
 524 S S H E T G F I Q Y L D S G I W  
  
 1951 CACTTGGCTTTACAATGACGGAAAGGAGTCAGAAGTGGTTCTTCT  
 540 H L A F Y N D G K E S E V V S F L

1 GAATTGGGACAGCCTCTCCCTGCCGCCGCTGCTGCTGCCGCCGCCACCGCCGGCTGGTCCCTCCCTGCTTT  
 76 TACTTCTCTGCATGACAGTTGTTTCTTCATCTGAGCAGACACCAGCTTCAGATGCTCGAGGTGAGAAACATGC  
 151 CTTTCAGTTGGCTACTGGTTACTTAATTAAATCAGCCGGCAGCTCCGTGATCTATTTCGTCCCTGTCCCTCT  
 226 TGACGAGCCCGGGATGGTTGGAGTAGCATTAAAGAACTAGAAAAGTGGCCAGAAACAGCAGCTAAAGAAT  
 301 TATTACGATATACTTGATTTGAGTTGCTAGGAGCTTCTTCCCCCTGATCTTCTGAACCTTCTTGAG  
 376 TTTTAATAATGGCTTGGACTTGGACATTGGACATTGATTTCTGGAGGTGAGCCGATGGAGATTTCAG  
 451 CCTCTGCGTGGTAATGGACCGTGAGAGCCGGCAGGCCCTTCTGGAGGTGAGCCGATGGAGATTTCAG  
 1 M E I Y S P D  
 526 ACATGTCTGAGGTGCGCCGAGAGGTCTCCAGCCCTCCACTCAGCTGAGTCAGACCCATCTTGATGGC  
 8 M S E V A A E R S S S P S T Q L S A D P S L D G L  
 601 TTCCGGCAGCAGAAGACATGCCAGAGCCCCAGACTGAAGATGGAGAACCCCTGGACTCGTGGCCCTGGCGTG  
 33 P A A E D M P E P Q T E D G R T P G L V G L A V P  
 676 CCTGCTGCGTGCCTAGAACGCTGAGCCCTGAGAGGTTGCCCTCAACTCAGAGAAAATCTGCATTGTC  
 58 C C A C L E A E R L R G C L N S E K I C I V P I L  
 751 TGGCTTGCCTGGTCAGCCTCTGCCCTGATGCCGCCCTCAAGTGGGTTATTGAGACAAGATCTTGAATATG  
 83 A C L V S L C L C I A G L K W V F V D K I F E Y D  
 826 ACTCTCCTACTCACCTTGACCCCTGGGGGTTAGGCCAGGACCTATTATTCTCTGGACCCA  
 108 S P T H L D P G G L G Q D P I I S L D A T A A S A  
 901 CTGTTGGGTGCGTCTGAGGCATAACACTCACCTGTCTCTAGGGCTCAATCTGAAAGTGGAGGTCAG  
 133 V W V S S E A Y T S P V S R A Q S E S E V Q V T V  
 976 TGCAAGGTGACAAGGCTGTTGCTCCTTGAAACCATCAGGGCACCGAACCGAAGAACGTT  
 158 Q G D K A V V S F E P S A A P T P K N R I F A F S  
 1051 CTTCTTGCGCTTCACTGCGCCATCTTCCCTCACCCACCCGGAACCCCTGAGGTGAGAACGCC  
 183 F L P S T A P S F P S P T R N P E V R T P K S A T  
 1126 CTCAGCCACAAACAGAAACTAATCTCCAAACTGCTCCTAAACTTCTACATCTACATCC  
 208 Q P Q T T E T N L Q T A P K L S T S T S T T G T S  
 1201 GCCATCTTGAAAATGTGGAGAAGGAGAAAACCTTCTGTGTGAATGGAGGGAGTGCTTC  
 233 H L V K C A E K E K T F C V N G G E C F M V K D L  
 1276 TTTCAAAACCCCTGAGATACTTGCAAGTCCCCAAATGAGTTACTGGTGTGATCGCTGCC  
 258 S N P S R Y L C K C P N E F T G D R C Q N Y V M A  
 1351 CCAGCTTCTACAGTACGTCCACTCCCTTCTGTCTCGCTGAATAGGAGCATGCTCAG  
 283 S F Y S T S T P F L S L P E O  
 1426 GTTGTGCGATCTCCCTCAGATTCCACCTAGAGCTAGATGTGTCTTAC  
 1501 GTCCGATGAGAACATTAACAAAGCAATTGTATTACTTCCTCTGTTCCGACTAG  
 1576 GGTGTGAGGCTCCGGATGTTCTGAAATTGATATTGATGTGATACAAATTGATAGTCA  
 1651 TGAAATATGATAATAAGGCATTCAAGTCTCACTTTATTGATAAAATCATTCTACT  
 1726 TCTCTTTATACAAATGACCACATCCTGAAAAGGGTGTGCTAAGCTGTA  
 1801 AGTTAATTTGATTCAAGATGTGTTATTGTCACAAATAACATAATAAGGAAAA  
 AAAAAACCGAATTGATGGTA

EGF-like

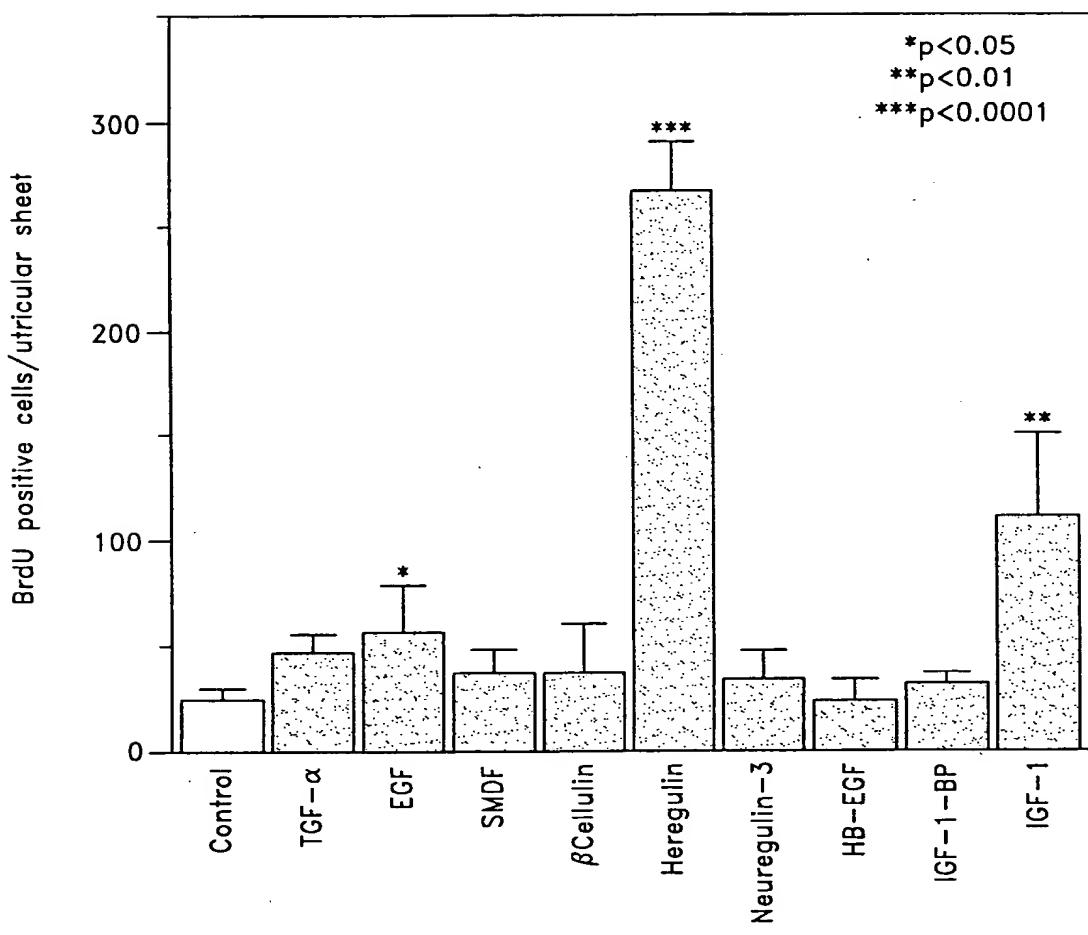


FIG. 9

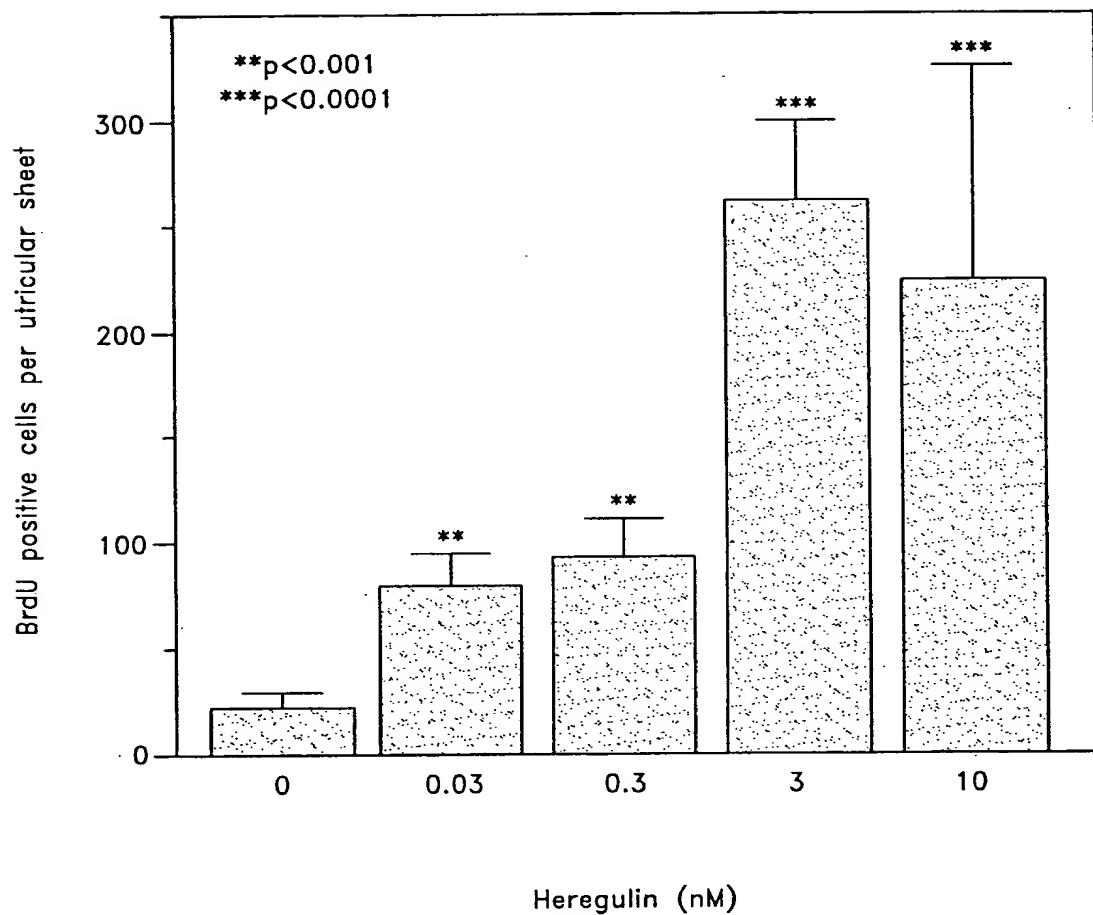


FIG. 10

Heregulin increases the number of 3H-thymidine labeled cells in supporting and hair cell layers in gentamicin-treated utricles

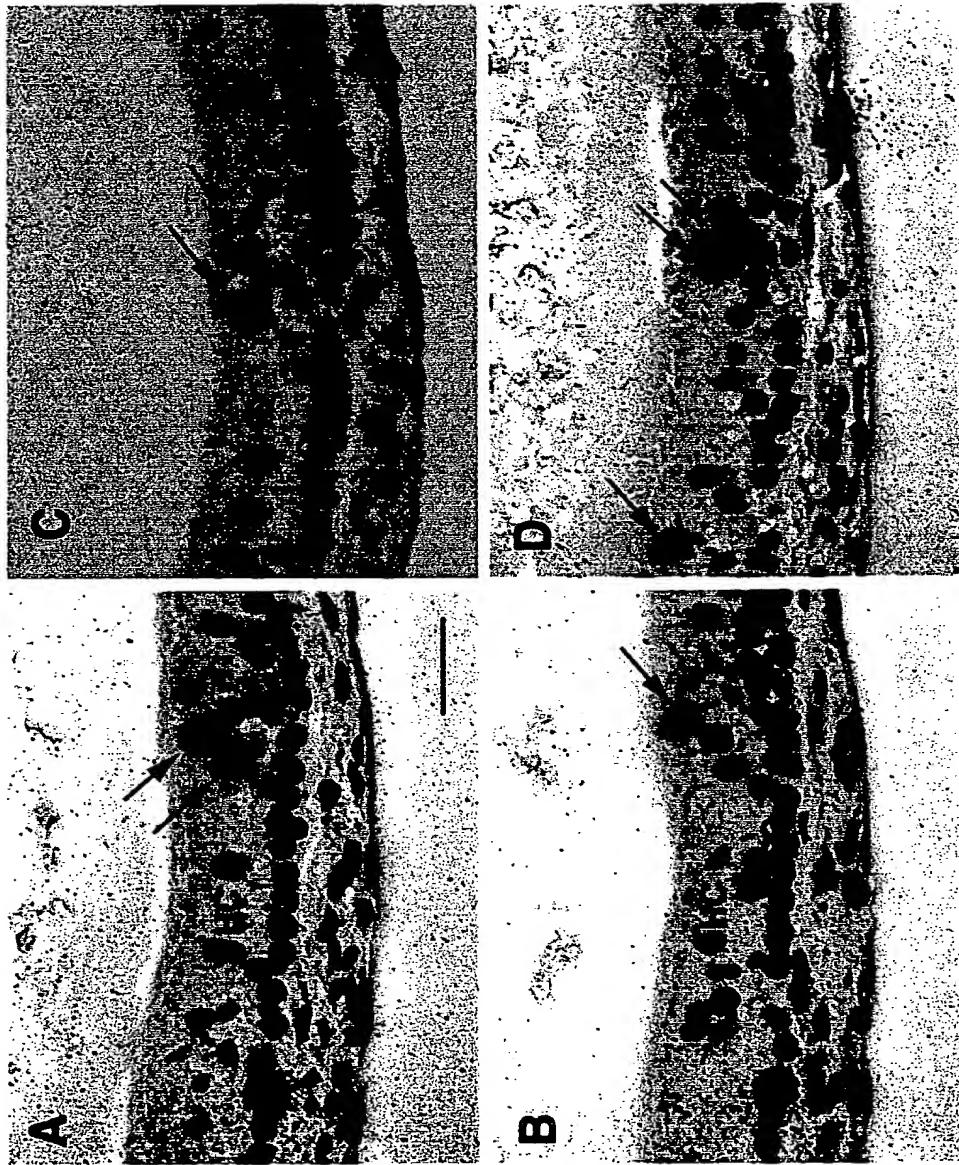


FIG. 11

Heregulin Enhances the Numbers of  $^3\text{H}$ -thymidine Labeled Cells in Both Supporting and Hair Cell Layers

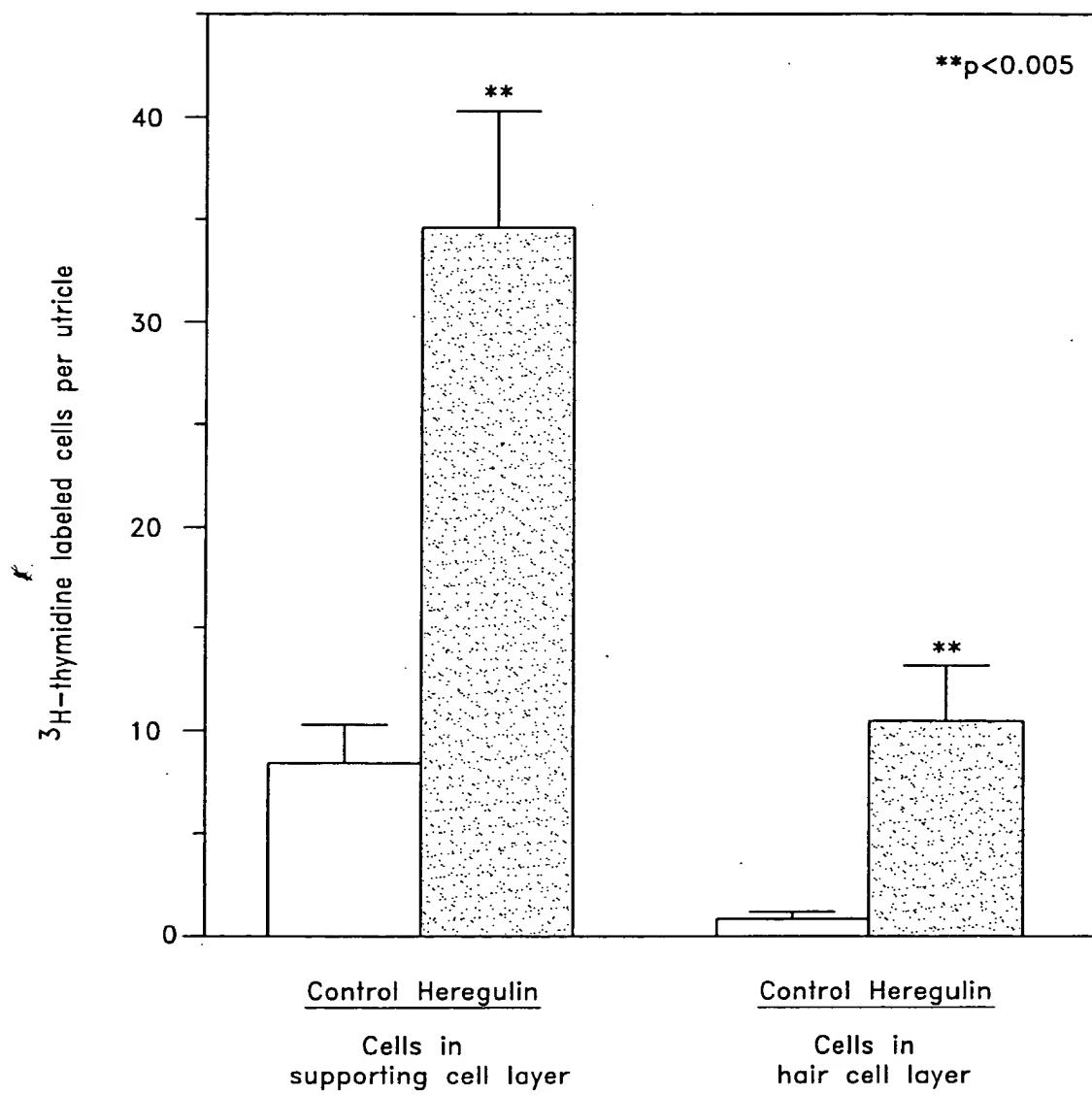


FIG. 12

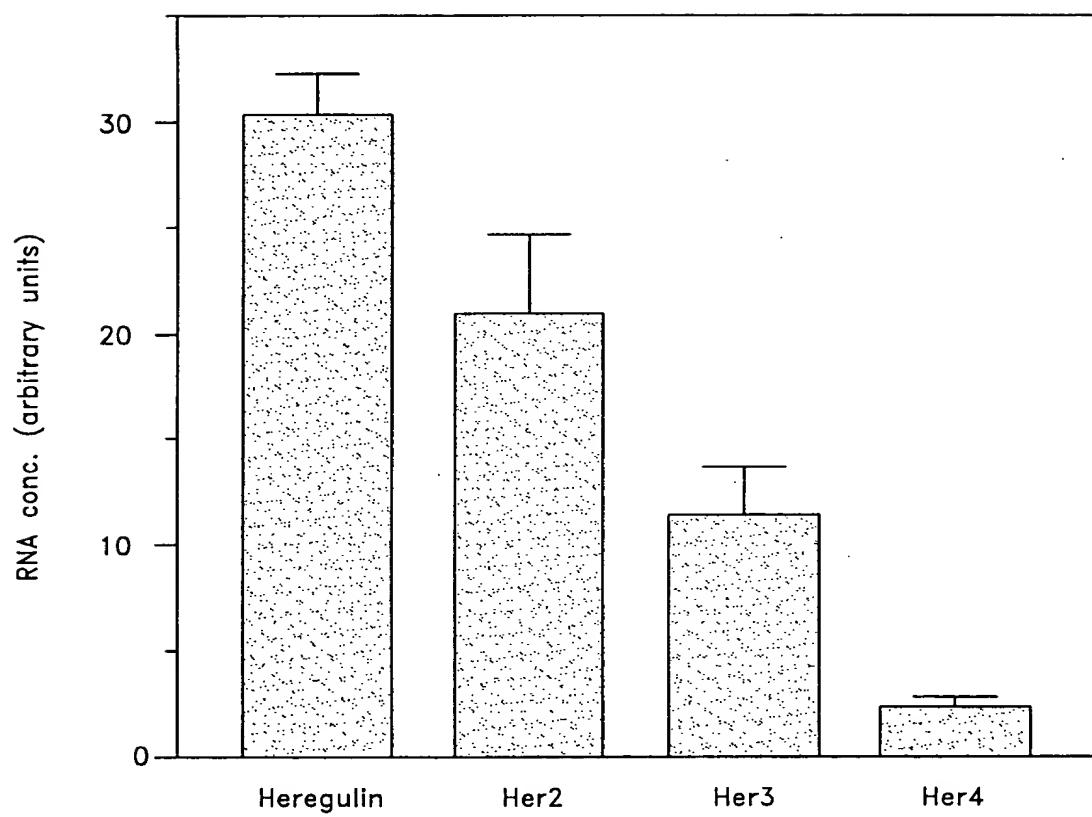


FIG. 13

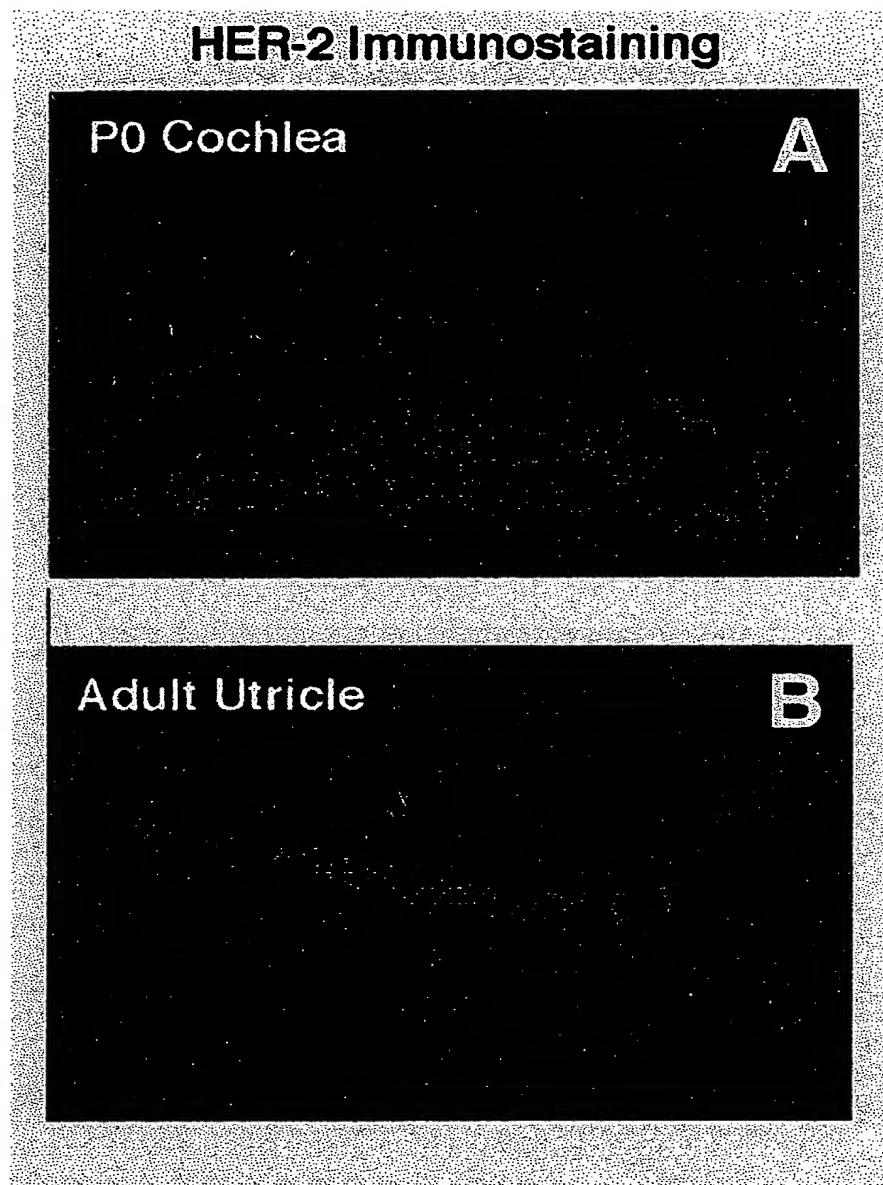


FIG.14